

RAW SEQUENCE LISTING

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Application Serial Number: 10/786,478A
Source: FW9
Date Processed by STIC: 12/16/04

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RAW SEQUENCE LISTING DATE: 12/16/2004
PATENT APPLICATION: US/10/786,478A TIME: 15:22:27

Input Set : A:\PRD2045NP-US.Subst.Seq.List.txt
Output Set: N:\CRF4\12162004\J786478A.raw

3 <110> APPLICANT: Chen, Jingcai
4 Kuei, Chester
5 Liu, Changlu
6 Lovenberg, Timothy W.
7 Sillard, Rannar
8 Sutton, Steven W.
10 <120> TITLE OF INVENTION: RELAXIN3-GPCR135 COMPLEXES AND THEIR PRODUCTION AND USE
12 <130> FILE REFERENCE: PRD2045NP-US
14 <140> CURRENT APPLICATION NUMBER: US 10/786,478A
15 <141> CURRENT FILING DATE: 2004-02-25
17 <150> PRIOR APPLICATION NUMBER: US 60/451,702
18 <151> PRIOR FILING DATE: 2003-03-04
20 <160> NUMBER OF SEQ ID NOS: 28
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 40
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Primer
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37 <211> LENGTH: 39
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51 <213> ORGANISM: Artificial
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54 <223> OTHER INFORMATION: Primer
56 <400> SEQUENCE: 3
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60 <210> SEQ ID NO: 4
61 <211> LENGTH: 41
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial
65 <220> FEATURE:

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 142 ggcattcatta tcttgcgtt cctgtgtgttca tggccgaccg cggcgccgcg 900
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150	caggagtatt	tcctgtgcca	ggtataacgcg	ttccctgtga	gcgtgtgcct	agcgcaactcc	1140
152	aacagctgcc	tcaaccccg	cctctactgc	ctcgtgcgccc	gcgaggcc	caaggcgctc	1200
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156	actaccaagc	cgaggcacga	ggatcagggg	ctgcaggccc	cgccggcc	ccacgcggcc	1320
158	gcggagccgg	acctgctcta	ctaccaccc	ggcgtcgtgg	tctacagccg	ggggcgctac	1380
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173	gcgtcgctgc	agcttcagga	tctgtgggtgg	gagctggggc	tagatgtgcc	agacgggtgc	180
175	gcgcctggc	atccctccggg	tggcggcgcc	gcagagagca	cagacactga	ggccagggtta	240
177	cgatcctca	tcagcgcgg	ttactgggtg	gttgtgccc	tgggactggc	cgcaacctg	300
179	ctggttctct	acctgatgaa	gagcaagcaa	ggctggcga	aatcctccat	caacctcttt	360
181	gtcaactaacc	tggcactgac	tgactttcag	ttcgtgctca	ctctgcccctt	ttgggctgtg	420
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187	taccactcgg	tggcctcg	tctcaagagc	catcggacc	gagggcgtgg	cggtggcgac	600
189	tgctcgcc	agagcttgc	ggagagctgc	tgttttcag	ccaaggtgc	gtgtgggtt	660
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228	gttgcaca	ggagcagca	tgcgtcgct	cagttcagg	acttgcgtt	ggagctgggg	180
230	ctggagttgc	ccgacgggtgc	ggcgcctgg	catccccgg	gcagcgg	ggcagagagc	240
232	gcggacacag	aggccagggt	acggatc	atcagcgc	tttactgggt	gtttgtgc	300
234	ctgggactgg	ctggcaaccc	gctgttctc	tacatgt	agagcaaaca	gggctggc	360
236	aaatcctcca	ttaacctt	tgtcaactac	ctggcgt	ctgacttca	gtttgtgc	420
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256	agtacagccg ggcgtcgag acgttcaag gtcaccaagt cggtgaccat cgtagtcctt	1020
258	tccttcttct tatgttggct gcccaaccaa ggcgtcaccat cctggagcat cctcatcaag	1080
260	ttcaacgttag tgcccttca gtcaggatgtt ttcagtgc aagtgtacgc gttcccagt	1140
262	agcgtgtgcc tggcacactc caacagctgc ctcaacccca tccttactgt ctttagtgcgc	1200
264	cgcgaggcc gcaaggcgct caagaacctg ctgtggcgta tagcatcgcc ttcgctcacc	1260
266	agcatgcgc ctttaccgc caccaccaag ccagaacctg aagatcacgg gtcgaggcc	1320
268	ctggcggccac ttaatgttac tgcagagctt gacctgtatct actatccacc cgggtgtgg	1380
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283	gctgcgtgc agtttcagga ttgtgggg gagctggggc tggagggtcc cgacgggtgc	180
285	gcccctggc atccccccggg cagcgggtgg gcaagagacg cggacacaga ggccagggt	240
287	cgatctca tcagcgcgtt ttactgggtt gtttgcctt tggactggc tggcaacctt	300
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315	caggagttact ttcatgttca agtgcgtcg ttcccgttca gctgtgcctt ggcacactcc	1140
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321	accaccaagg cagaacctga agatcacggg ctgcaggccc tggcgccact taatgttact	1320
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 343 Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
 344 35 40 45
 347 Trp Trp Glu Leu Gly Leu Gly Leu Pro Asp Gly Ala Pro Pro Gly His
 348 50 55 60
 351 Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val
 352 65 70 75 80
 355 Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu
 356 85 90 95
 359 Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp
 360 100 105 110
 363 Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp
 364 115 120 125
 367 Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu
 368 130 135 140
 371 Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met
 372 145 150 155 160
 375 Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met
 376 165 170 175
 379 Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg
 380 180 185 190
 383 Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp
 384 195 200 205
 387 Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu
 388 210 215 220
 391 Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys
 392 225 230 235 240
 395 Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu
 396 245 250 255
 399 Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val
 400 260 265 270
 403 Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu
 404 275 280 285
 407 Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly
 408 290 295 300
 411 Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
 412 305 310 315 320
 415 Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
 416 325 330 335
 419 Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
 420 340 345 350
 423 Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
 424 355 360 365
 427 Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,18,19,20,21,22,23,24,25,26,27,28

VERIFICATION SUMMARY

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